

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Biogen, Inc.
(B) STREET: 14 Cambridge Center
(C) CITY: Cambridge
(D) STATE: Mass
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02142

(A) NAME: Roy R. Lobb
(B) STREET: 62 Loring Street
(C) CITY: Westwood
(D) STATE: Mass
(E) COUNTRY: USA
(F) POSTAL CODE (ZIP): 02090

(ii) TITLE OF INVENTION: Treatment for Asthma

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00030

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 821768
(B) FILING DATE: 13-JAN-1992

(2) INFORMATION FOR SEQ ID NO:1:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(1x) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy
chain variable region; amino acid 1 is Glu (E) but Gln (Q)
may be substituted"

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTC	AAA	CTG	CAG	CAG	TCT	GGG	GCA	GAG	CTT	GTG	AAG	CCA	GGG	GCC	TCA	48
Val	Lys	Leu	Gln	Gln	Ser	Gly	Ala	Glu	Leu	Val	Lys	Pro	Gly	Ala	Ser	
2				6					11					16		
GTC	AAG	TTG	TCC	TGC	ACA	GCT	TCT	GGC	TTC	AAC	ATT	AAA	GAC	ACC	TAT	96
Val	Lys	Leu	Ser	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	Lys	Asp	Thr	Tyr	
			21					26					31			
ATG	CAC	TGG	GTG	AAG	CAG	AGG	CCT	GAA	CAG	GGC	CTG	GAG	TGG	ATT	GGA	144
Met	His	Trp	Val	Lys	Gln	Arg	Pro	Glu	Gln	Gly	Leu	Glu	Trp	Ile	Gly	
		36					41					46				
AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	CCG	AAG	TTC	CAG	192
Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	Pro	Lys	Phe	Gln	
	51					56					61					
GTC	AAG	GCC	ACT	ATT	ACA	GCG	GAC	ACG	TCC	TCC	AAC	ACA	GCC	TGG	CTG	240
Val	Lys	Ala	Thr	Ile	Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Trp	Leu	
66					71					76					81	
CAG	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	ACT	GCC	GTC	TAC	TAC	TGT	GCA	288
Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
				86					91					96		
GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	TTC	TGG	GGC	CAA	336
Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	Phe	Trp	Gly	Gln	
			101					106					111			
GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA									360
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser									
			116				121									

(2) INFORMATION FOR SEQ ID NO:2:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(11) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
2 6 11 16

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
21 26 31

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
36 41 46

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
51 56 61

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
66 71 76 81

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
86 91 96

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
101 106 111

Gly Thr Thr Val Thr Val Ser Ser
116 121

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "HP1/2 light chain variable region"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT	ATT	GTG	ATG	ACC	CAG	ACT	CCC	AAA	TTC	CTG	CTT	GTT	TCA	GCA	GGA	48
Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly	
1				5					10					15		
GAC	AGG	GTT	ACC	ATA	ACC	TGC	AAG	GCC	AGT	CAG	AGT	GTG	ACT	AAT	GAT	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
			20					25					30			
GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
	50					55					60					
AGT	GGA	TAT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
65					70					75					80	
GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
				85				90						95		
ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
			100					105								

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp
			20					25					30		
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35					40					45			
Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly
	50					55					60				

Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala
65					70					75					80
Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr
				85					90						95
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile						
			100					105							

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